

In the Specification:

At the top of page 1, following the Title, please insert the following:

--CROSS REFERENCE TO RELATED APPLICATIONS

This application is a U.S. National Stage application of International Application No. PCT/EP03/04546 filed April 25, 2003.

BACKGROUND OF THE INVENTION--

On page 1, after the first full paragraph, please insert the heading:

-- SUMMARY OF THE INVENTION --

On page 2, after the seventh full paragraph, please insert the heading:

-- BRIEF DESCRIPTION OF THE FIGURES --

On page 6, after the first full paragraph, please insert the heading:

-- DETAILED DESCRIPTION OF THE INVENTION --

On page 25 of the Specification, please amend Table 2 as follows:

Table 2 Y-Chromosomal STSs			
STS	Left Primer	Right Primer	Product
SKY1	GGACATTTGGCTGCAGAGAT (SEQ ID NO: 1)	TGGCAATGCACTCTCATCAT (SEQ ID NO: 2)	255
SKY2	TCAGGACAGACAGGCTGCTA (SEQ ID NO: 3)	CCTGCCACTGAGCTCCTTAC (SEQ ID NO: 4)	~1700
SKY3	TTCTCCCTCATCTTCCAAGC (SEQ ID NO: 5)	GCTTCCATCCATTAGCAAGG (SEQ ID NO: 6)	167
SKY4	CCTTTCATTCCATTCTCTTCCA (SEQ ID NO: 7)	CGCACTTTATGGACTGCAA (SEQ ID NO: 8)	111
SKY5*	CCCTCGTCCATTTCTTTTGA (SEQ ID NO: 9)	CCTCGAATTTAATGGATTGC (SEQ ID NO: 10)	202
SKY6*	TCAATGGATGCACAGTGTGGC (SEQ ID NO: 11)	TCCACTGAATTCCATTGCAC (SEQ ID NO: 12)	328
SKY7	GGGAGTGCAAAGGGAAAGAT (SEQ ID NO: 13)	CTTCCATGGGGTGACATTC (SEQ ID NO: 14)	223
SKY8	CCATTCATTCGAGTTCATTACG (SEQ ID NO: 15)	ATTGGAATGGAATCGGACAG (SEQ ID NO: 16)	189
SKY9	GGCCGATGGTCAAAGTGTTA (SEQ ID NO: 17)	GAAACGGGCTCTGAAATTCT (SEQ ID NO: 18)	531
SKY10*	ATAAGGGGCAGGTTTGTAC (SEQ ID NO: 19)	GCTACTTATTCAGTGTTTAACTGACAC (SEQ ID NO: 20)	329
SKY11*	AAAGTGGGTGAAGGACATGG (SEQ ID NO: 21)	TTTTTGTTTGTGGCAGGTG (SEQ ID NO: 22)	469
SKY12*	TTGAGTCACTGGGGATAACTG (SEQ ID NO: 23)	TATGGCCCACAATCACTTCA (SEQ ID NO: 24)	216
SKY13*	GGCAGCCTAGAAAGTCTTGTC (SEQ ID NO: 25)	CCCTTGGGATTTTGTCTGTT (SEQ ID NO: 26)	198

Markers indicated with a * amplify DNA fragments from more than one genomic locus (see Chapter *Restriction analysis of PCR products* for detail.)

On page 28 of the Specification, please amend Table 5 as follows:

Table 5 Genomic primer pairs for microdeletion screening in adult males with idiopathic short stature

Primer Sequence (5' → 3')		product size	primer	Genomic Location*	
Forward	reverse			forward	reverse
ATTCCACCGAAACCCATTT (SEQ ID NO: 27)	CTCCCCTACCACCAACACAC (SEQ ID NO: 28)	251	<u>A72</u>	72300-72318	72549-72530
AGGGCCCTCACATGATTA (SEQ ID NO: 29)	GCGACACCATTTCTTTCCAT (SEQ ID NO: 30)	255	<u>A92</u>	91949-91968	92204-92185
GACATCGTGGTGTCTGTTGC (SEQ ID NO: 31)	CAGACGTTGTTTCAGGTCGTG (SEQ ID NO: 32)	232	A111	111509-111528	111740-111721
GCACCATTAGTGCGCTTGT (SEQ ID NO: 33)	TTCTCCCTTTACCCCAAATTC (SEQ ID NO: 34)	269	<u>A134</u>	134542-134560	134810-134790
CCAGCAGGAGTCTTGGAGTC (SEQ ID NO: 35)	TGAGAGGCACCTACGGTTAGA (SEQ ID NO: 36)	250	<u>A158</u>	157911-157930	158160-158140
CCAAGCATGCCTTCCTAAAG (SEQ ID NO: 37)	TGCCTTCTCATCTGCTTGTG (SEQ ID NO: 38)	147	B17	17598-17617	17744-17725
ATCCTGGGAGATGCATCAGA (SEQ ID NO: 39)	TGAGTCCTAAACCGTACACATACA (SEQ ID NO: 40)	209	B37	37406-37425	37614-37591
CAATGGAAATGTTGCAGGTG (SEQ ID NO: 41)	TCCTGCCCTGCTGTTAGAGT (SEQ ID NO: 42)	158	<u>B59</u>	59871-59890	60028-60009
GCAAGGGTGTGCAAGTTTA (SEQ ID NO: 43)	TGCATATTGTCCACACATGG (SEQ ID NO: 44)	360	<u>B82</u>	82128-82147	82487-82468
AAAGAGAAGGGCCCTGTGAT (SEQ ID NO: 45)	CTAGGCAACAGCACTGGAAA (SEQ ID NO: 46)	239	<u>B102</u>	102854-102873	103092-103073
AAAATCCAACCTCCCAAGTG (SEQ ID NO: 47)	GCAAGAATCTGGGCTCTCAC (SEQ ID NO: 48)	353	C17	17307-17326	17659-17640
CACTGGGGAAGGCTGTGATA (SEQ ID NO: 49)	CATTGTCATCACTGCCAGGT (SEQ ID NO: 50)	339	C37	37271-37290	37609-37590
CCCACTTCTTCTCCAAAGTCC (SEQ ID NO: 51)	GCACCCGTTTTCCTGATCTA (SEQ ID NO: 52)	139	C56	56159-56179	56297-56278
GGGGCATATTCTACACACCAA (SEQ ID NO: 53)	TGAAATGGCAAACCTTTCAGA (SEQ ID NO: 54)	495	C77	76731-76751	77225-77205
AAGAATGGAAGGATCTCCAAGA (SEQ ID NO: 55)	TCTGTGCAGAAATGATGGATTC (SEQ ID NO: 56)	342	C97	96759-96780	97100-97079
TGGTAGTGGGAAACTGCTCA (SEQ ID NO: 57)	TGGTGTGCTAAGTGGCTGTC (SEQ ID NO: 58)	144	C120	120709-120728	120852-120833
GCTGCAGTTAGCTAAACCAAGAC (SEQ ID NO: 59)	ATTCTGCCTGAACCTCCAGA (SEQ ID NO: 60)	162	C142	142289-142311	142450-142431

On page 29 of the specification, please amend Table 6 as follows:

Table 6 Sequences of isolated exon trap clones

Exon trap clones:

Name	Sequence (5'→3')	Size (bp)	Orientation
et_a_001	GGTCTTTGGCTCAACTCAGGTTCCCTCTACCTGAAATGATCCACCTTC AGAGAATTGGATG (SEQ ID NO: 61)	61	reverse
et_a_002	CTGTGTTGCCTCCTCGATGGGAAAAGAAACAAGCGCACTAATGGTG CATTT (exon 1) (SEQ ID NO: 62) CTGGAGCATCAGGGGTGTCTTCTATGATCAAGGAAGGAAGCCACTC AGGGTGATAGAGCTGCAGACTTCTGCTTGGTCA CTCTGATAGCTCTGGGAACACTGTGCACCTCTCTGGCTGTGATGGGG AAACT (exon 2) (SEQ ID NO: 63)	182	reverse
et_a_003	CTTTTACATAGAATGGTAACTCCTTTTGCACCTCGTGTTTTTC (SEQ ID NO: 64)	44	forward
et_a_004	AAAGTTGGTAGTTTCGCTCCCGGGCTGATGCTCAGAGTGTGGAACCTTG AGGAGCTGCGGTGACATCCTGCAGCCACACGGGAGGTGGCTCCTCA GGGGCGATTGCTGGCTGTGTCAACCACAGGGGACACCGGGCACAGC TTGAAGCTTGGGGACAGGGAGCTGAGAGGCAC (SEQ ID NO: 65)	171	reverse
et_c_001	GATTACATGGACTACTATATTTAAATTCCTTCTAAACTTTTTCCCAT TTCTGCTCAATTTTCATTCTCCAATATTTGCAAACTTAAAGTTC (SEQ ID NO: 66)	93	forward
et_c_002	GCTGAACATTATTTCTTTATTCCAGATTAGAGGACTAGGATTCATGG GATTATGCATCAA (SEQ ID NO: 67)	60	forward
et_c_003	GGAAATCTTGAAATGGCAAACCTTTCAGAAGAGATGGCAGAGACTC TCCTACATATTCTGTTCTCAAT (SEQ ID NO: 68)	68	reverse
et_c_004	ACACTGGAAGAATTGGTGTCTAGGCAGTCTGGGATAATAGCCTAGTT CTAAGGACATTATCATTGATCCCTTATAGGCCATAGACCTCCAT (exon 1) (SEQ ID NO: 69) TTCTTCCTGTTGGTGCAGGAGGGTGATTAAGGGCTTTTCCTACCTTA AGTTGATCAAAGTGGTATTTTCATAAGATTAATCTGGCAGCAGAATG CA (exon 2) (SEQ ID NO: 70)	188	reverse
et_c_005	CTTGGTTGGGAAAATATGGCCACCATATTGCTGGGAAAGCCACCAA GAGTGGACTGTTACCAATATCCAAGGGACATGA (SEQ ID NO: 71)	79	forward

On page 30 of the Specification, please amend Table 7A as follows:

Table 7A Primer Pairs for predicted genes

Primer pairs for predicted genes		product size ¹	predicted gene	restriction enzyme ²	Genomic location ³	
Forward	reverse				forward	reverse
GCTTGGAACTTGAGGTGCTC (SEQ ID NO: 72)	GGAGATGTGGGCTTGTGAGT (SEQ ID NO: 73)	482	a_r001		104600-104581	103332-103351
CTGTGGGTGCATTAGGTGTG (SEQ ID NO: 74)	CTGGTACATGCTGCCTGCT (SEQ ID NO: 75)	841	a_r_002		144939-144920	111361-111379
GACCTCTTTTGAGAAAGTCAGCA (SEQ ID NO: 76)	AAAGCAATGGCAACAAAAGC (SEQ ID NO: 77)	446	b_f_001		30214-30236	61274-61255
AGAGGGAGGAAAGAGCCATC (SEQ ID NO: 78)	GTTGTACGGGCTGCAGAATC (SEQ ID NO: 79)	790	b_r_001		25244-25225	762-781
TGAGTCCTAAACCGTACACATACA (SEQ ID NO: 80)	TTTCTGTGCGTGAGAACACA (SEQ ID NO: 81)	122	b_r_002		37614-37591	29995-30014
TCTCTGTGGTGCTGATCCTG (SEQ ID NO: 82)	GCAAGAATCTGGGCTCTCAC (SEQ ID NO: 83)	730	c_f_001		6243-6262	17659-17640
ATCCCTATTCGCCCTTAGA (SEQ ID NO: 84)			c_f_001b		10734-10753	
ACCTCAGGGTGACGCTTTTA (SEQ ID NO: 85)	TGAGCAGTTTCCCACTACCA (SEQ ID NO: 86)	350	c_f_002	Bsh1236I	80230-80249	120728-120709
GCTGCAGTTAGCTAAACCAAGAC (SEQ ID NO: 87)	TTCTGCAAGGGTCTGGTTCT (SEQ ID NO: 88)	123	c_f_003	A1wI	142289-142311	162171-162152
CACAGAAGCCAGGGATCG (SEQ ID NO: 89)	GCATCTCGCCCTTTCCTC (SEQ ID NO: 90)	1150	c_r_001	BamHI	6361-6344	2888-2905
CAACACTGTACACCGCAACA (SEQ ID NO: 91)	TTCTCCAAAGTCCGATACCTG (SEQ ID NO: 92)	172	c_r_002	BspMI	81022-81003	56167-56187
TGGAGACATTCAACGTCAA (SEQ ID NO: 93)	TGGTAGTGGGAACTGCTCA (SEQ ID NO: 94)	325	c_r_003	A1uI	129988-129968	120709-120728
AGCTGCCTGACTTCTTGGAA (SEQ ID NO: 95)	CTTGCCACACCTTGATCTC (SEQ ID NO: 96)	574	c_r_004	AccI	170431-170412	162765-162784
CGTGCTGGATTCTTATTG (SEQ ID NO: 97)	CCCACTTCTTCTCCAAAGTCC (SEQ ID NO: 98)	212	c_r_005	MspI	66318-66299	56159-56179

¹predicted product size in bp; ² Potential Y-derived transcript copies will be cut with the indicated restriction enzyme, potential X-derived transcripts remain uncut; ³ indicates primer positions (orientation centromere to telomere) in the predicted gene containing BAC (a, b, c, or d).

On page 31 of the Specification, please amend Table 7B as follows:

Table 7B Primer Pairs for Y copy of Adlican

Primer sequence (5'→3')	Direction with respect to putative transcription orientation	primer
<u>GACTCCTGGCCTTGACTTGA (SEQ ID NO: 99)</u>	forward	AdlYEx1
<u>TCTCTGTGGTGCTGATCCTG (SEQ ID NO: 100)</u>	forward	cfl
<u>GGAGGAGCAAAAACAAGAAGAGA (SEQ ID NO: 101)</u>	forward	cfl-117
<u>ACTGATGAGCACGGGAACC (SEQ ID NO: 102)</u>	forward	cfl-205
<u>TCCATCCTGAAAGTGCCTG (SEQ ID NO: 103)</u>	forward	C17c
<u>ACATGTATACATGCTGCCAA (SEQ ID NO: 104)</u>	forward	C18
<u>CAGCGAAGGAAAGCACATT (SEQ ID NO: 105)</u>	forward	AdlYEx5
<u>GGCGACCTGAAGGGGACT (SEQ ID NO: 106)</u>	forward	cfl-1915
<u>CTGTCCAGTCCTCAGGAAGC (SEQ ID NO: 107)</u>	forward	C21
<u>GAAGCATCCACCAAAGCG (SEQ ID NO: 108)</u>	forward	cfl-4679
<u>ACAGCGGGCGCTATGAGT (SEQ ID NO: 109)</u>	forward	cfl-4a
<u>CAGGATCAGCACACAGAGA (SEQ ID NO: 110)</u>	reverse	AdlYEx2
<u>CTGGGGAAGTTGGATTTTCTC (SEQ ID NO: 111)</u>	reverse	C17b
<u>ACCAGGTTCCCGTGCTCA (SEQ ID NO: 112)</u>	reverse	cfl-227
<u>GCAAGAATCTGGGCTCTCAC (SEQ ID NO: 113)</u>	reverse	cfl
<u>ACTGTGATTCCCACCGTGAT (SEQ ID NO: 114)</u>	reverse	C17c
<u>TTGTTTTGAGGAACGCCTCT (SEQ ID NO: 115)</u>	reverse	C18
<u>GGATGTGGGATCTGGTGAG (SEQ ID NO: 116)</u>	reverse	cfl-2079
<u>GGGTGTAATTTTCTCCATTG (SEQ ID NO: 117)</u>	reverse	AdlYEx5
<u>CGTCCGTTTCAGCAGTGACA (SEQ ID NO: 118)</u>	reverse	cfl-4810
<u>CTGACGTCCGTCCTCTGC (SEQ ID NO: 119)</u>	reverse	cfl-4b
<u>ATGGACAGTGATCCGGTTTC (SEQ ID NO: 120)</u>	reverse	cfl-6453
<u>TGAGCTGCACGATCAACCTC (SEQ ID NO: 121)</u>	reverse	cfl-6559

On page 32 of the Specification, please amend Table 7C as follows:

Table 7C Rt-PCR primer sequences for ADLY

Primer	Sequence (5'→3')	Pos. in ADLY	Pos. in ADLX	ADL exon ²
<i>Forward Primer</i>				
AdlYEx1	GACTCCTGGCCTTGACTTGA (SEQ ID NO: 122)	44-63	--	1
cfl	TCTCTGTGGTGCTGATCCTG (SEQ ID NO: 123)	184-203	184-203	2
AdlYEx5	CAGCGAAGGAAAGCACATTT (SEQ ID NO: 124)	2177-2196	--	5
C21	CTGTCCAGTCCTCAGGAAGC (SEQ ID NO: 125)	5089-5108	5620-5639	5
CFL-4A	ACAGCGGGCGCTATGAGT (SEQ ID NO: 126)	5971-5988	6502-6519	6
<i>Reverse Primer</i>				
AdlYEx2	CAGGATCAGCACACAGAGA (SEQ ID NO: 127)	203-184	203-184	2
cfl	GCAAGAATCTGGGCTCTCAC (SEQ ID NO: 128)	914-895	1435-1416	5
AdlYEx5	GGGTGTAATTTTCTCCCATTTG (SEQ ID NO: 129)	3103-3083	--	5
cfl-4b	CTGACGTCCGTCCTCTGC (SEQ ID NO: 130)	6143-6126	6631-6614	6
cfl-6453	ATGGACAGTGATCCGGTTTC (SEQ ID NO: 131)	7158-7139	7649-7630	7

¹ADLY refers to the gene predicted according to homology comparison with function X-adlican. ²Numbering of exons is based on the exon/intron organization of the X-copy. Please note: RT-PCR with cfl for/rev would generate different-sized products from adlican copies. cfl-4a/cfl-6453 and C21/Cfl-4b amplification products encompass chromosome –specific restriction sites (cfl-4a/cfl-6453; Y-BamHI, X-PstI; C21/cfl-4b; Y-NlaIII, X-SacI).

On page 33 of the Specification, please amend Table 8 as follows:

Table 8 RT-PCR primer sequences for exon trap clones

Exon trap clone	Forward Primer	Reverse Primer
eta2	GCACCATTAGTGCCTTGT (SEQ ID NO: 132) a: TTACATAGAATGGTAACTCCTTTTGC (SEQ ID NO: 134) b: AACTCCTTTTGCACCTCGTG (SEQ ID NO: 135)	GAGCATCAGGGGTGTCTTCT (SEQ ID NO: 133)
eta3		a: GCTGATGCTCAGAGTGTGGA (SEQ ID NO: 136) b: GATTGCTGGCTGTGTCACC (SEQ ID NO: 137)
eta4	a: TTTAAAATTCCTTCTAACTTTTCC (SEQ ID NO: 138) b: CCCATTTCTGCTCAATTTTCA (SEQ ID NO: 139) a: GCTGAACATTATTTCTTTATTCCAGA (SEQ ID NO: 140) b: AGAGGACTAGGATTCATGGGATT (SEQ ID NO: 141)	
etc1		a: TGAAATGGCAAACCTTTCAGA (SEQ ID NO: 142) b: GGCAGAGACTCTCCTACATATTC (SEQ ID NO: 143)
etc2	TGGCCTATAAAGGGATCAATG (SEQ ID NO: 144) a: GAAAGCCACCAAGAGTGGAC (SEQ ID NO: 146) b: ACCAATATCCAAGGGACATGA (SEQ ID NO: 147)	GGTGCAGGAGGGTGATTAAG (SEQ ID NO: 145)
etc3		
etc4		
etc5		

The product size of eta2 is 175bp and of etc4 166bp. For single exon-trap clones semi-nested PCR was carried out: a reflects the outer primer, b the inner one.

On page 34 of the Specification, please amend Table 9b as follows:

Table 9b Exon/intron boundaries of conserved exons

Exon	Intron/Exon		Exon/Intron	
	ADLX	ADLY	ADLX	ADLY
1	GAGCTGCCTC (SEQ ID NO: 148)	GAGCTGCCTC (SEQ ID NO: 149)	CCAAGGACAGgtgaggac cc (SEQ ID NO: 158)	CCAAGGATAGgtgaggaccc (SEQ ID NO: 159)
2	tctacctcagGTATCCGAGA (SEQ ID NO: 150)	tctacctcagGTATCCGAGA (SEQ ID NO: 151)	TCAATTTGGGgtttgtacca (SEQ ID NO: 160)	TCAATTTGGGgtttgtacca (SEQ ID NO: 161)
5	ttgttttagGAATTCTGAA (SEQ ID NO: 152)	ttgttttagGAATTCTGAA (SEQ ID NO: 153)	GTTTCCACAGgtaatatgtt (SEQ ID NO: 162)	GTTTCCACATgtaagattt (SEQ ID NO: 163)
6	ttttctccagGAGCTCTTAT (SEQ ID NO: 154)	ttttctccagGAGTTCTTAT (SEQ ID NO: 155)	CGCTCTTCAGgtaggcagct (SEQ ID NO: 164)	CGCTTTTCAGgtaggcagct (SEQ ID NO: 165)
7	ttttctgtagTTTTGATAGC (SEQ ID NO: 156)	ttttctgtagTTTTGATAGT (SEQ ID NO: 157)	ATATTCTCCCC (SEQ ID NO: 166)	ATATTCTCCCC (SEQ ID NO: 167)